

FIG. 1(a)

1
ATGACACAACCGCATCGTCTCGTGTAGTCTTTGATCCAGCAACCCACCATTTTCG
-----+-----+-----+-----+-----+-----+-----+
TACTGTGTGGCGTAGCAGAGCACATCAGAAACTAGGTCGTTGGGTGGTGTAAAGC
MetThrGlnProAlaSerSerArgValValPheAspProSerAsnProThrThrPheSer
M T Q P A S S R V V F D P S N P T T P S
60

61
GTGGAAGCAATTGCGGCTTACACCCCGTTGCTTTAATACGACTTTTAAACGCCAGTGGA
-----+-----+-----+-----+-----+-----+-----+
CACCTTCGTTAACGCCGAATGTGGGGCAACGAAATTATGCTGAAAAATTTGCGGTACCT
ValGluAlaIleAlaAlaTyrThrProValAlaLeuIleArgLeuLeuAsnAlaSerGly
V E A I A A Y T P V A L I R L L N A S G
120

121
CCTTTGCAACCTGTGTACCGTGTGGACATCGCTGATGCCAGAGCATTTACACCGTGGGA
-----+-----+-----+-----+-----+-----+-----+
GGAACGTTGGACCAAGTGGCACACCTGTAGCGACTACGGTCTTCGTAATGTGGCACCT
ProLeuGlnProGlyHisArgValAspIleAlaAspAlaArgSerIleTyrThrValGly
P L Q P G H R V D I A D A R S I Y T V G
180

181
GCCGCGGCAGTGCCGCGTGCACGCGCTAACCATTAATGCAAAATACGATACGCCGAACG
-----+-----+-----+-----+-----+-----+-----+
CGCGCGCGGTACGCGCGCACGTGCGCGATTGGTATTACGTTTATGCTATGCGGCTTGC
AlaAlaAlaSerAlaAlaArgAlaArgAlaAsnHisAsnAlaAsnThrIleArgArgThr
A A A S A A R A R A N H N A N T I R R T
240

241
GCCATGTTTGCCGAGACTGACCCCTATGACATGTTAAGACCACCGTTGGCTTAAACCGT
-----+-----+-----+-----+-----+-----+-----+
CGGTACAAACGGCTCTGACTGGGATACTGTACCAATTCTGGTTGCCAACCGAATTTTGCA
AlaMetPheAlaGluThrAspProMetThrTrpLeuArgProThrValGlyLeuLysArg
A M F A E T D P M T W L R R P T V G L K R
300

FIG. 1(b)

301 ACGTTTAACCCGCGTATTATACGACCACAAACCCCAATCCATCCATGAGTTTGGAATC
-----+-----+-----+-----+-----+-----+
TGCAAAATTGGCGCATATAATGCTGGTGTGGGGTTAGGTAGTACTCAAACCCCTTAG
ThrPheAsnProArgIleIleArgProGlnProProAsnProSerMetSerLeuGlyIle
T F N P R I I R P Q P P N P S M S L G I
360

361 TCGGGCCCTACTATATTCGCCGCAAAAACACAGAGCGCCGATCAGTCTGCTTTACAACAG
-----+-----+-----+-----+-----+-----+
AGCCCCGGATGATATAACGCGCTTTTGTGTCTCGCGCTAGTCAGACGAAATGTTGTC
SerGlyProThrIleLeuProGlnLysThrGlnSerAlaAspGlnSerAlaLeuGlnGln
S G P T I L P Q K T Q S A D Q S A L Q Q
370

421 CCCGCCGCGTTGGCGTTTTCGGGATCATCCCCCGCAACACCCCCCACCCTCAAACGACGTCG
-----+-----+-----+-----+-----+-----+
GGCGCGCAACCGCAAAAGCCCTAGTAGGGCGTGTGGGGGTGGAGTTTGCTGCAGC
ProAlaAlaLeuAlaPheSerGlySerSerProGlnHisProProGlnThrThrSer
P A A L A F S S S P Q H P P P P Q T T S
430

481 GCATCCGTTGGACAACAGCAACACGTTGTCGGGGTCTTCTGGACAACAACCCGCAACAG
-----+-----+-----+-----+-----+-----+
CGTAGGCAACCTGTTGTCGTTGTGCACCAACAGCCCCCAGAACCTGTTGTCGCTGTC
AlaSerValGlyGlnGlnGlnHisValValSerGlySerSerGlyGlnGlnProGlnGln
A S V G Q Q Q H V V S G S S G Q Q P Q Q
490

541 GGAGCACAGTCAAGCACTGTCCAGCCCAACAACCGGATCACCGCCCGCGGCCCAAGCGGTG
-----+-----+-----+-----+-----+-----+
CCTCGTGTACAGTTCGTGACAGTTCGGTTGTTGGCTAGTGGCGGCGCGGTTCCGCAC
GlyAlaGlnSerSerThrValGlnProThrThrGlySerProProAlaAlaGlnGlyVal
G A Q S S T V Q P T T G S P P A A Q G V
550

FIG. 1(c)

```
601 CCACAGTCTACCCCGCCCCCAACCCCAAAATACCCCCCAGGGGGTAAGGACAGACCTTG
-----+-----+-----+-----+-----+-----+
GGTGTTCAGATGGGCGGGGTTGGGTTTATGGGGGTCCCCCATTCCTGTCTGGAAC
ProGlnSerThrProProProThrGlnAsnThrProGlnGlyGlyLysGlyGlnThrLeu
P Q S T P P P T Q N T P Q G G K G Q T L 660

661 TCACACACGGGACAAATCTGGAAACGCTTCAAGAAGTCGTAGGGTG
-----+-----+-----+-----+-----+-----+
AGTGTGTGCCCTGTAGACCTTTGCGAAGTTCTTCAGCATCCCAC
SerHisThrGlyGlnSerGlyAsnAlaSerArgSerArgVal
S H T G Q S G N A S R S R R V 705
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FIG. 2

NO.	STATUS	ELISA IgM REF- ERENCE	ELISA IgM pMal- VP26* 1µm/ml	ELISA IgM pQE- VP26* 1µg/ml	NO.	STATUS	ELISA IgM REF- ERENCE	ELISA IgM pMal- VP26* 1µm/ml	ELISA IgM pQE- VP26* 1µg/ml
		CONJ. 1:50	CONJ. 1:50	CONJ. 1:25			CONJ. 1:50	CONJ. 1:50	CONJ. 1:25
		SERUM 1:42	SERUM 1:168	SERUM 1:168			SERUM 1:42	SERUM 1:168	SERUM 1:168
1	-	11	86	62	29	-	16	19	104
2	-	22	38	100	30	-	8	13	44
3	-	16	31	72	31	-	3	23	47
4	-	57	23	88	32	-	50	23	101
5	+	133	399	88	33	-	9	32	117
6	-	0	161	118	34	+	250	187	204
7	-	10	28	77	35	+	291	1079	470
8	-	47	45	60	36	-	26	52	44
9	-	7	16	63	37	+	139	66	123
10	+	132	173	160	38	-	38	87	49
11	-	71	117	70	39	-	26	25	40
12	-	0	32	75	40	-	49	13	63
13	-	17	75	66	41	-	5	20	34
14	-	11	16	57	42	-	27	43	80
15	-	23	27	73	43	-	51	49	161
16	-	11	27	59	44	-	8	38	100
17	+	979	1720	532	45	-	21	38	133
18	-	9	18	44	46	-	10	33	82
19	-	34	30	71	47	-	29	18	35
20	+	293	630	215	48	-	30	66	97
21	+	126	139	259	49	-	21	35	97
22	-	61	277	169	50	-	56	64	82
23	+	292	808	154	51	-	5	40	56
24	+	581	98	115	52	-	97	55	37
25	+	321	821	304	53	-	2	19	35
26	+	509	519	375	54	-	31	21	39
27	+	298	>2500	694					
28	-	29	36	29					

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FIG. 3

NO.	STATUS	ELISA IgG REF- ERENCE	ELISA IgG pMal- VP26* 1µm/ml	ELISA IgG pQE- VP26* 2µg/ml	NO.	STATUS	ELISA IgG REF- ERENCE	ELISA IgG pMal- VP26* 1µm/ml	ELISA IgG pQE- VP26* 2µg/ml
		CONJ. 1:50	CONJ. 1:50	CONJ. 1:50			CONJ. 1:50	CONJ. 1:50	CONJ. 1:50
		SERUM 1:231	SERUM 1:100	SERUM 1:100			SERUM 1:231	SERUM 1:100	SERUM 1:100
1	+	1014	176	137	28	+	549	89	172
2	+	302	87	356	29	-	34	87	120
3	+	642	97	314	30	-	76	55	128
4	+	612	87	0	31	-	0	38	101
5	+	1383	181	215	32	-	41	94	116
6	+	930	132	118	33	-	8	147	177
7	+	653	39	145	34	+	1315	860	340
8	+	915	47	469	35	+	1629	282	187
9	+	570	23	220	36	+	469	218	287
10	+	1770	131	253	37	+	693	181	346
11	+	990	104	76	38	+	1449	296	169
12	+	698	227	335	39	+	1139	85	193
13	+	141	62	501	40	+	1509	64	118
14	+	338	39	44	41	+	457	110	159
15	+	556	113	246	42	+	343	304	545
16	+	791	45	423	43	+	1455	511	244
17	+	2982	264	258	44	+	1030	174	245
18	+	1205	192	295	45	+	528	50	184
19	+	694	80	100	46	+	510	161	353
20	+	1143	270	340	47	+	300	94	290
21	+	1405	377	256	48	+	490	91	157
22	+	539	42	72	49	+	888	348	277
23	+	2449	533	530	50	+	1301	83	195
24	+	1923	1117	620	51	+	704	247	139
25	+	1420	95	54	52	+	2523	2325	757
26	PRIMARY	1194	277	66	53	+	447	99	153
	+				54	+	848	149	167
27	ZOSTER	2087	341	204					
	+								

Figure 1(a)

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Figure 1(b)

```

ACGTTTAACCCGCGTATTATACGACCAACACCCCAATCCATCCATGAGTTTGGGAATC
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
TGCAAATGGGGCCATAATATGCTGCTGTTGGGGGTTTAGGTAGGTACTCAAACCTTAG
ThrPheAsnProArgIleIleArgProGlnProProAsnProSerMetSerLeuGlyIle
T: P N P R I I R P Q P P N P S M S L G I

TCGGGGCTACTATATTGCCGCAAAAACACAGAGCGCGATCAGTCTGCTTTACACAG
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
AGCCCCGGATGATATAACGGCGTTTTTTGTGTCTCGCGGCTAGTCAGACGAAATGTTGTC
SerGlyProThrIleLeuProGlnLysThrGlnSerAlaAspGlnSerAlaLeuGlnGln
S G P T I L P Q K T Q S A D Q S A L Q Q

CCCCCGCGTTGGCGTTTTTCGGGATCATCCCCGCAACCCCCCACCTCAAACGACGTGG
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
GGCGCGCGCAACCGCAAAAGCCCTAGTAGGGCGCTTGTGGGGGTGGAGTTTGTCTGCAGC
ProAlaAlaLeuAlaPheSerGlySerSerProGlnHisProProProGlnThrThrSer
P A A L A F S G S S P Q H P P P Q T T S

GCATCGGTTGGACAACAGCAACACGTCGTCGGGCTCTTCGGACAACACCGCAACAG
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
CGTAGGCAACCTGTGTGCTGTGTGCACCACAGCCCAGAAACCTGTGTGTGGCGTTGTC
AlaSerValGlyGlnGlnGlnHisValValSerGlySerSerGlyGlnGlnProGlnGln
A S V G Q Q Q H V V S G S S G Q Q P Q Q

GGAGCAGACTCAAGCACTGTCCAGCCAACAACCGATCACCGCCCGGGCCCAAGGCGTG
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
CCTCGTGTCACTTCGTACAGGTCGGTTGTTGGCTTAGTGGGGGGCCCGGTTCCGCAC
GlyAlaGlnSerSerThrValGlnProThrThrGlySerProProAlaAlaGlnGlyVal
G A Q S S T V Q P T T G S P P A A Q G V

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CCACAGTCTACCCCGCCCCCAACCCAAATAACCCCTCAGGGGGGTAAAGGGACAGACCTTG
601 -----+-----+-----+-----+-----+-----+-----+
GGTGTGAGATGGGGCGGGGGTTCGGTTTATGGGGGTCCCCCAATCCCTGTCTGGAAAC
ProGlnSerThrProProProThrGlnAsnThrProGlnGlyGlyLysGlyGlnThrLeu
P; Q S T P P P T Q N T P Q G G K G Q T L

TCACACGGGACAACTCGGAACGCTTCAGAAGTGTAGGGTG
661 -----+-----+-----+-----+-----+-----+-----+ 705
AGTGTGTGCCCTGTTAGACCTTTGCGAAGTCTCTCAGCATCCCAAC
SerHisThrGlyGlnSerGlyAsnAlaSerArgSerArgArgVal
S H T G Q S G N A S R S R R V

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Figure 2

Met Thr Gln Pro Ala Ser Ser Arg Val Val Phe Asp Pro Ser Asn Pro
Thr Thr Phe Ser Val Glu Ala Ile Ala Ala Tyr Thr Pro Val Ala Leu
Ile Arg Leu Leu Asn Ala Ser Gly Pro Leu Gln Pro Gly His Arg Val
Asp Ile Ala Asp Ala Arg Ser Ile Tyr Thr Val Gly Ala Ala Ala Ser
Ala Ala Arg Ala Arg Ala Asn His Asn Ala Asn Thr Ile Arg Arg Thr
Ala Met Phe Ala Glu Thr Asp Pro Met Thr Trp Leu Arg Pro Thr Val
Gly Leu Lys Arg Thr Phe Asn Pro Arg Ile Ile Arg Pro Gln Pro Pro
Asn Pro Ser Met Ser Leu Gly Ile Ser Gly Pro Thr Ile Leu Pro Gln
Lys Thr Gln Ser Ala Asp Gln Ser Ala Leu Gln Gln Pro Ala Ala Leu
Ala Phe Ser Gly Ser Ser Pro Gln His Pro Pro Pro Gln Thr Thr Ser
Ala Ser Val Gly Gln Gln Gln His Val Val Ser Gly Ser Ser Gly Gln
Gln Pro Gln Gln Gly Ala Gln Ser Ser Thr Val Gln Pro Thr Thr Gly
Ser Pro Pro Ala Ala Gln Gly Val Pro Gln Ser Thr Pro Pro Pro Thr
Gln Asn Thr Pro Gln Gly Gly Lys Gly Gln Thr Leu Ser His Thr Gly
Gln Ser Gly Asn Ala Ser Arg Ser Arg Arg Val #

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Figure 3

No.	Status	ELISA	ELISA	ELISA	No.	Status	ELISA	ELISA	ELISA
		IgM	IgM	IgM			IgM	IgM	IgM
		Reference	pMal- VP26*	pQE- VP26*			Reference	pMal- VP26*	pQE- VP26*
		1:50	1:50	1:25			1:50	1:50	1:25
		Serum	Serum	Serum			Serum	Serum	Serum
		1:42	1:168	1:168			1:42	1:168	1:168
1	-	11	86	62	29	-	16	19	104
2	-	22	38	100	30	-	8	13	44
3	-	16	31	72	31	-	3	23	47
4	-	57	23	88	32	-	50	23	101
5	+	133	399	88	33	-	9	32	117
6	-	0	161	118	34	+	250	187	204
7	-	10	28	77	35	+	291	1079	470
8	-	47	45	60	36	-	26	52	44
9	-	7	16	63	37	+	139	66	123
10	+	132	173	160	38	-	38	87	49
11	-	71	117	70	39	-	26	25	40
12	-	0	32	75	40	-	49	13	63
13	-	17	75	66	41	-	5	20	34
14	-	11	16	57	42	-	27	43	80
15	-	23	27	73	43	-	51	49	161
16	-	11	27	59	44	-	8	38	100
17	+	979	1720	532	45	-	21	38	133
18	-	9	18	44	46	-	10	33	82
19	-	34	30	71	47	-	29	18	35
20	+	293	630	215	48	-	30	66	97
21	+	126	139	259	49	-	21	35	97
22	-	61	277	169	50	-	56	64	82
23	+	292	808	154	51	-	5	40	56
24	+	581	98	115	52	-	97	55	37
25	+	321	821	304	53	-	2	19	35
26	+	509	519	375	54	-	31	21	39
27	+	298	>2500	694					
28	-	29	36	29					

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Figure 4

No.	Status	ELISA	ELISA	ELISA	No.	Status	ELISA	ELISA	ELISA
		IgG	IgG	IgG			IgG	IgG	IgG
		Reference	pMal	pQE			Reference	pMal	pQE
			VP26*	VP26*				VP26*	VP26*
			1 µg/ml	2 µg/ml				1 µg/ml	2 µg/ml
		Conj.	Conj.	Conj.			Conj.	Conj.	Conj.
		1:50	1:50	1:50			1:50	1:50	1:50
		Serum	Serum	Serum			Serum	Serum	Serum
		1:231	1:100	1:100			1:231	1:100	1:100
1	+	1014	176	137	28	+	549	89	172
2	+	302	87	356	29	-	34	87	120
3	+	642	97	314	30	-	76	55	128
4	+	612	87	0	31	-	0	38	101
5	+	1383	181	215	32	-	41	94	116
6	+	930	132	118	33	-	8	147	177
7	+	653	39	145	34	+	1315	860	340
8	+	915	47	469	35	+	1629	282	187
9	+	570	23	220	36	+	469	218	287
10	+	1770	131	253	37	+	693	181	346
11	+	990	104	76	38	+	1449	296	169
12	+	698	227	335	39	+	1139	85	193
13	+	141	62	501	40	+	1509	64	118
14	+	338	39	44	41	+	457	110	159
15	+	556	113	246	42	+	343	304	545
16	+	791	45	423	43	+	1455	511	244
17	+	2982	264	258	44	+	1030	174	245
18	+	1205	192	295	45	+	528	50	184
19	+	694	80	100	46	+	510	161	353
20	+	1143	270	340	47	+	300	94	290
21	+	1405	377	256	48	+	490	91	157
22	+	539	42	72	49	+	888	348	277
23	+	2449	533	530	50	+	1301	83	195
24	+	1923	1117	620	51	+	704	247	139
25	+	1420	95	54	52	+	2523	2325	757
26	Primary	1194	277	66	53	+	447	99	153
	+				54	+	848	149	167
27	Zoster	2087	341	204					
	+								

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Met Thr Gln Pro Ala Ser Ser Arg Val Val Phe Asp Pro Ser Asn Pro

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1 5 10 15
Thr Thr Phe Ser Val Glu Ala Ile Ala Ala Tyr Thr Pro Val Ala Leu
20 25 30
Ile Arg Leu Leu Asn Ala Ser Gly Pro Leu Gln Pro Gly His Arg Val
35 40 45
Asp Ile Ala Asp Ala Arg Ser Ile Tyr Thr Val Gly Ala Ala Ala Ser
50 55 60
Ala Ala Arg Ala Arg Ala Asn His Asn Ala Asn Thr Ile Arg Arg Thr
65 70 75 80
Ala Met Phe Ala Glu Thr Asp Pro Met Thr Trp Leu Arg Pro Thr Val
85 90 95
Gly Leu Lys Arg Thr Phe Asn Pro Arg Ile Ile Arg Pro Gln Pro Pro
100 105 110
Asn Pro Ser Met Ser Leu Gly Ile Ser Gly Pro Thr Ile Leu Pro Gln
115 120 125
Lys Thr Gln Ser Ala Asp Gln Ser Ala Leu Gln Gln Pro Ala Ala Leu
130 135 140
Ala Phe Ser Gly Ser Ser Pro Gln His Pro Pro Pro Gln Thr Thr Ser
145 150 155 160
Ala Ser Val Gly Gln Gln Gln His Val Val Ser Gly Ser Ser Gly Gln
165 170 175
Gln Pro Gln Gln Gly Ala Gln Ser Ser Thr Val Gln Pro Thr Thr Gly
180 185 190
Ser Pro Pro Ala Ala Gln Gly Val Pro Gln Ser Thr Pro Pro Pro Thr
195 200 205
Gln Asn Thr Pro Gln Gly Gly Lys Gly Gln Thr Leu Ser His Thr Gly
210 215 220
Gln Ser Gly Asn Ala Ser Arg Ser Arg Arg Val
225 230 235

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Varicella-Zoster-Virus
(B) STRAIN: Ellen

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGACACAAC CCGCATCGTC TCGTGTAGTC TTTGATCCCA GCAACCCAC
CACATTTTCG 60

GTGGAAGCAA TTGCGGCTTA CACCCCGTT GCTTTAATAC GACTTTTAA
CGCCAGTGGA 120

CCTTTGCAAC CTGGTCACCG TGTGGACATC GCTGATGCCA GAAGCATTTA
CACCGTGGGA 180

GCCGCGGCCA GTGCCGCGCG TGCACGCGCT AACCATAATG CAAATACGAT
ACGCCGAACG 240

GCCATGTTTG CCGAGACTGA CCCTATGACA TGGTTAAGAC CAACGGTTGG
CTTAAACGT 300

ACGTTTAACC CGCGTATTAT ACGACCACAA CCCCCAAATC CATCCATGAG
TTGGGAATC 360

TCGGGGCCTA CTATATTGCC GCAAAAAACA CAGAGCGCCG ATCAGTCTGC
TTTACAACAG 420

CCCGCCGCGT TGGCGTTTTC GGGATCATCC CCGCAACACC CCCCACCTCA
AAGACGTCG 480

GCATCCGTTG GACAACAGCA ACACGTGGTG TCGGGTCTT CTGGACAACA
ACCGCAACAG 540

GGAGCACAGT CAAGCACTGT CCAGCCAACA ACCGGATCAC CGCCCGCGGC
CCAAGGCGTG 600

CCACAGTCTA CCCC GCCCCC AACCCAAAAT ACCCCCAGG GGGGTAAGGG
ACAGACCTTG 660

TCACACACGG GACAATCTGG AAACGCTTCA AGAAGTCGTA GGGTG
705

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(A) DESCRIPTION: /desc = "Synthetische DNA"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Varicella-Zoster-Virus

(B) STRAIN: Ellen

(viii) POSITION IN GENOME:

(B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGAATTCCGG ATGACACAAC CCGCATCGTC TCGTGTA

37

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetische DNA"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Varicella-Zoster-Virus

(B) STRAIN: Ellen

(viii) POSITION IN GENOME:

(B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GCTCTAGATT ACACCCTACG ACTTCTTGAA GCGTTTCC

38

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetische DNA"

(iii) HYPOTHETICAL: NO

09874140-060601

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Varicella-Zoster-Virus
- (B) STRAIN: Ellen

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGAATTCCGC GCCTGCAGGT CGACACTAGT GGAT

34

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetische DNA"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Varicella-Zoster-Virus
- (B) STRAIN: Ellen

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCTCTAGATT ACACCCTACG ACTTCTTGAA GCGTTTCC

38

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetische DNA"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Varicella-Zoster-Virus
- (B) STRAIN: Ellen

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

27

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(viii) POSITION IN GENOME:

(B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

38

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